

SEQUENCE LISTING

<110> Genencor International, Inc.
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 Harding, Fiona A.
 Schellenberger, Volker

<120> CAB Molecules

<130> GC822-PCT

<140> PCT/US2004/041429

<141> 2004-12-10

<150> US 60/529,354

<151> 2003-12-12

<150> US 60/577,255

<151> 2004-04-06

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<170> PatentIn version 3.2

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 20 25 30

Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 35 40 45

Xaa Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
 50 55 60

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 85 90 95

Xaa Xaa Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Xaa Xaa Xaa
 100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala
 145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Thr Ser Asn Leu Ala Ser Xaa Xaa
 180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

195

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln
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Arg Ser Ser Tyr Pro Leu Thr
 225 230

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Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
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Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
 50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
 130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro

370

375

380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
 385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
 405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
 420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
 435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
 450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
 465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
 485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
 500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
 515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
 530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
 545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
 565 570 575

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Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
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35 40 45

Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser
50 55 60

Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg
65 70 75 80

Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu
85 90 95

Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr
100 105 110

Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn
115 120 125

Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro
130 135 140

Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala
145 150 155 160

Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr
165 170 175

Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro

180

185

190

Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala
195 200 205

Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys
210 215 220

Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala Asn Met Ala Pro
225 230 235 240

Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln
245 250 255

Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu
260 265 270

Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe
275 280 285

Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro
290 295 300

Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly
305 310 315 320

Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile
325 330 335

Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala
340 345 350

Ala Tyr His Ile Leu Glu Ala Leu Gln
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20 25 30

Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Gly Leu Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Xaa Xaa Xaa

100

105

110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala
 145 150 155 160

Ser Ser Ala Val Tyr Ala Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa
 180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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 35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly

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Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
 290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
 305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
 325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
 340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
 355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
 370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
 385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
 405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
 420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
 435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
 450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
 465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
 485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
 500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
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Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
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Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys

85

90

95

Asn Glu Gly Leu Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
 130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
 145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
 165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
 180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
 225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
 245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro Gly Met
 260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
 275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
 290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
 305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

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20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ala Val Tyr Ala Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Asp Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
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Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
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Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
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Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ala Val Tyr Ala Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Lys Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
 385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
 405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
 420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
 435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
 450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
 465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
 485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
 500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
 515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
 530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
 545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys
 565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
 580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
 595 600 605

<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 protein fragment

<400> 11

Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Thr
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
 195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
 210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
 225 230 235 240

Lys Arg Ala Ala

<210> 12
 <211> 5178
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic pME27.1 plasmid sequence

<400> 12
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 gggacctcag tcaagttgtc ctgcacagct tctggcttca acattaaaga ctcttatatg 180
 cactggttga ggcagggggc tgaacagggc ctggagtgtga ttggatggat tgatcctgag 240
 aatggtgata ctgaatatgc cccgaagtgc cagggaagg ccacttttac tacagacaca 300
 tctccaaca cagcctacct gcagctcagc agcctgacat ctgaggacac tgcgtcttat 360
 tattgtaatg aggggactcc gactggggcg tactactttg actactgggg ccaagggcgc 420
 acggtcaccg tctcctcagg tggaggcggg tcaggcggag gtggctctgg cggtggcgga 480
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 accataacct gcagtgccag ctcaagtgtg agttacatgc actggttcca gcagaagcca 600
 ggcacttctc ccaaaactctg gatttatagc acatccaacc tggcttctgg agtccctgct 660
 cgcttcagtg gcagtggtatc tgggacctct tactctctca caatcagcgg aatggaggct 720
 gaagatgctg ccacttatta ctgccagcaa agatctagtt acccactcac gttcggtgct 780
 ggcaccaagc tggagctgaa acgggcgggc acaccggtgt cagaaaaaca gctggcggag 840
 gtggtcgcca atacgattac cccgctgatg aaagcccagt ctgttccagg catggcgggtg 900
 gccgttattt atcagggaac accgcactat tacacatttg gcaaggccga tatcgcggcg 960

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aagctttcta gattaagg 5178

<210> 13
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 heavy chain sequence

<400> 13

Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Ser Gly Thr
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 14
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 linker sequence

<400> 14

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 15
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1 light chain sequence

<400> 15

Glu Asn Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Ala Thr
100 105 110

<210> 16

<211> 360

<212> PRT

<213> Artificial Sequence

<220>

<223> BLA protein fragment

<400> 16

Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val Ala Asn Thr Ile Thr
1 5 10 15

Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met Ala Val Ala Val Ile
20 25 30

Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala
35 40 45

Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile
50 55 60

Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly
65 70 75 80

Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr
85 90 95

Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr Thr
100 105 110

Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn Ala
115 120 125

Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro Gly
130 135 140

Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly Leu Phe Gly Ala Leu
145 150 155 160

Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr Arg
165 170 175

Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys
180 185 190

Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val
195 200 205

Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr
210 215 220

Asn Val Gln Asp Met Ala Asn Trp Val Met Ala Asn Met Ala Pro Glu
225 230 235 240

Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile Ala Leu Ala Gln Ser
245 250 255

Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met
260 265 270

Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val Glu Thr Ser Phe Gly
275 280 285

Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala
290 295 300

Pro Pro Val Lys Ala Ser Trp Val His Lys Thr Gly Ser Thr Gly Gly
305 310 315 320

Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val
325 330 335

Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala
340 345 350

Tyr His Ile Leu Glu Ala Leu Gln
355 360

<210> 17
<211> 605
<212> PRT

<213> Artificial Sequence

<220>

<223> SW149.5 protein

<400> 17

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 18
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1.1 protein variant

<400> 18

Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Val Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 19

<211> 1815

<212> DNA

<213> Artificial Sequence

<220>

<223> CAB1.2 variant coding sequence

<400> 19

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tctgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120

cctgaacagg gcctggagtg gattggatgg attgatcctg agaatgggtg tactgaatat 180

gcccgcgaagt tccagggcaa ggccactttt actacagaca cactctccaa cacagcctac 240

ctgcagctca gcagcctgac atctgaggac actgcctgtc attattgtaa tgaggggact 300

ccgactgggc cgtactactt tgactactgg ggccaaggga ccacgggtcac cgtctcctca 360

ggtggaggcg gttcaggcgg aggtggctct ggcgggtggcg gatcagaaaa tgtcgtcacc	420
cagtctccag caatctgtct tgcattctcca ggggagaagg tcaccataac ctgcagtgcc	480
agctcaagtg taagttacat gcaactggctc cagcagaagc caggcacttc tcccaaaactc	540
gtgatttata gcacatccaa cctggcttct ggagtcctcg ctgcgttcag tggcagtggga	600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tggcacttat	660
tactgccagc aaagatctag ttaccactc acgttcgggt ctggcaccac gctggagctg	720
aaacggggcg ccacacgggt gtcagaaaaa cagctggcgg aggtggtcgc gaatacgatt	780
accccgctga tgaaagccca gtctgttcca ggcattggcg tggccgttat ttatcaggga	840
aaaccgcaact attacacatt tggcaaggcc gatatcgcg cgaataaac cgttacgcct	900
cagacctgt tcgagctggg ttctataagt aaaaaccttca ccggcgcttt aggtggggat	960
gccattgctc gcggtgaaat ttcgtggac gatcgggtga ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcggc	1080
ctgccgctac aggtaccgga tgaggtcacg gataacgcct cctgctgcg cttttatcaa	1140
aactggcagc cgcagtgaa gcctggcaca acgcgtcttt acgccaacgc cagcatcggt	1200
ctttttggtg cgctggcggg caaaccttct ggcattgcc atgagcaggc catgacgacg	1260
cgggtcctta agccgctcaa gctggacct acctggatta acgtgccgaa agcggaaagag	1320
gcgcattacg cctggggcta tcgtgacggg aaagcggctg gcgtttcgcc gggtatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaactg ggtcatggca	1440
aacatggcgc cggagaacgt tgctgatgcc tcacttaagc agggcatcgc gctggcgcag	1500
tcgcgctact ggcgtatcgg gtcaatgtat cagggtctgg gctgggagat gctcaactgg	1560
cccgtaggag ccaacacggt ggtcgagacg agttttggt atgtagcact ggcgcgcttg	1620
cccgtaggag aagtgaatcc accggtccc ccggtcaaa cgctcctgggt ccataaaacg	1680
ggctctactg gcgggtttgg cagctacgtg gcctttatc ctgaaaagca gatcgggtatt	1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatatc	1800
ctcgaggcgc tacag	1815

<210> 20
 <211> 605
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> CAB1.2 protein variant

<400> 20

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln

210	215	220
Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu		
225	230	235 240
Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val		
	245	250 255
Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met		
	260	265 270
Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly		
	275	280 285
Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe		
	290	295 300
Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp		
305	310	315 320
Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr		
	325	330 335
Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp		
	340	345 350
Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu		
	355	360 365
Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro		
	370	375 380
Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly		
385	390	395 400
Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln		
	405	410 415
Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp		
	420	425 430
Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg		
	435	440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 21
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRs of CAB1.4 protein variant

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> X = any amino acid

<220>

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<221> MISC_FEATURE
<222> (36)..(49)
<223> X = any amino acid

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<220>
<221> MISC_FEATURE
<222> (110)..(158)
<223> X = any amino acid
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<220>
<221> MISC_FEATURE
<222> (191)..(222)
<223> X = any amino acid
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Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa
165 170 175

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr
225 230

<210> 22
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CDRs of CAb1.4 variant

<220>
<221> misc_feature
<222> (1)..(153)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (184)..(225)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (274)..(372)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (406)..(552)
<223> n = a,t,c, or g

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<220>
<221> misc_feature
<222> (583)..(627)
<223> n = a,t,c, or g

<220>
<221> misc_feature
<222> (649)..(744)
<223> n = a,t,c, or g

<400> 22
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nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnggcttca acattaaaga ctctatatg 180
cacnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnntggat tgatcctgag 240
aatggtgata ctgaatatgc cccgaagttc cagnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 300
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 360
nnnnnnnnnnnn nngggactcc gactgggccc tactactttg actacnnnnnn nnnnnnnnnnnn 420
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 480
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 540
nnnnnnnnnnnn nnagtgcagc ctcaagtgtg agttacatgc acnnnnnnnnn nnnnnnnnnnnn 600
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnngat acatccaacc tggcttctnn nnnnnnnnnnnn 660
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 720
nnnnnnnnnnnn nnnnnnnnnnnn nnnncagcaa agagatagtt acccactcac g 771

<210> 23
<211> 1815
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CAB1.4 variant

<400> 23
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tcttcgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120
cctgaacagg gcctggagtg gattggatgg attgactctg agaatggtag tactgaatat 180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac 240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgaggggact 300

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ccgactgggc cgtactactt tgactactgg ggccaaggga ccacggtcac cgtctcctca	360
gggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgtgctcacc	420
cagtctccag caatcgtgtc tgcactctca ggggagaagg tcaccataac ctgcagtgcc	480
agctcaagtg taagtacat gcactgggtc cagcagaagc caggcacttc tcccaaacctc	540
gtgatttatg atacatccaa cctggcttct ggagtcctcg ctgcgttcag tggcagtgga	600
tctgggacct ttactctct cacaatcagc cgaatggagg ctgaagatgc tggcacttat	660
tactgccagc aaagagatag ttaccactc acgttcgggt ctggcaccaa gctggagctg	720
aaacgggcgg ccacacccgt gtcagaaaaa cagctggcgg aggtggctgc gaatacgatt	780
accccgctga tgaaagccca gtctgttcca ggcatggcgc tggccgttat ttatcaggga	840
aaaccgcact attacacatt tggcaaggcc gatatcgcg cgaataaac cgttacgcct	900
cagaccctgt tcgagctggg ttctataagt aaaaccttca ccggcgcttt aggtggggat	960
gccattgtc ccggtgaaat ttcgctggac gatgcgggtga ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcggc	1080
ctgccgctac aggtaccgga tgaggtoacg gataacgcct ccctgctcgc cttttatcaa	1140
aactggcagc cgcagtgga gccctggaca acgcgtcttt accccaacgc cagcatcggt	1200
ctttttggtg cgctggcggt caaaccttct ggcatgcct atgagcaggc catgacgacg	1260
cgggtcctta agccgctcaa gctggaocat acctggatta acgtgccgaa agcgggaagag	1320
gcgcattacg cctggggcta tcgtgacggt aaagcgggtc gcgtttcgcc gggatatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaactg ggatcatgca	1440
aacatggcgc cggagaacgt tgcctgatgc tcacttaagc agggcatcgc gctggcgcag	1500
tcgcgctact ggcgatcgg gtcaatgtat cagggtctg gctgggagat gctcaactgg	1560
cccgtggagg ccaacacggt ggtcgagacg agttttggta atgtagcact ggcgccgttg	1620
cccgtggcag aagtgaatcc accggctccc ccggtcaaa cgtcctgggt ccataaaacg	1680
ggctctactg gcgggttttg cagctacgtg gcctttatct ctgaaaagca gatcggtatt	1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatatac	1800
ctcgaggcgc tacag	1815

<210> 24
 <211> 605
 <212> PRT

<213> Artificial Sequence

<220>

<223> CAB1.4 protein variant

<400> 24

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Asp Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys
565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
595 600 605

<210> 25
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CDRs of CAB1.6 variant

<220>
<221> misc_feature
<222> (1)..(153)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (184)..(225)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (274)..(372)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (406)..(552)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (583)..(627)

<223> n = a,t,c, or g

<220>

<221> misc_feature

<222> (649)..(744)

<223> n = a,t,c, or g

<400> 25

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nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 120

nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnggettca acattaaaga ctectatatg 180

cacnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnntggat tgatcctgag 240

aatggtgata ctgaatatgc cccgaagttc cagnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 300

nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 360

nnnnnnnnnnnn nngggctccc gactgggccc tactactttg actacnnnnnn nnnnnnnnnnnn 420

nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 480

nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 540

nnnnnnnnnnnn nnagtgccag ctcaagtgtg agttacatgc acnnnnnnnnn nnnnnnnnnnnn 600

nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnngat acatccaacc tggcttctnnn nnnnnnnnnnnn 660

nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 720

nnnnnnnnnnnn nnnnnnnnnnnn nnnncagcaa agagatagtt acccactcac g 771

<210> 26

<211> 1815

<212> DNA
<213> Artificial Sequence

<220>
<223> sequence encoding CAB1.6 protein variant

<400> 26
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tcttcgcacag cttctggctt caacattaaa gactcctata tgcactgggtg gaggcagggg 120
cctgaacagg gcctggagtg gattggatgg attgatcctg agaatggatg tactgaatat 180
gccccgaagt tccagggcaa ggccactttt actacagaca catcctccaa cacagcctac 240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgagggggctc 300
ccgactgggc cgtactactt tgactactgg ggccaaggga ccacggtcac cgtctcctca 360
gggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgcgtcacc 420
cagtcctcag caatcgtgtc tgcactctca ggggagaagg tcaccataac ctgcagtgcc 480
agctcaagtg taagttacat gcactgggtc cagcagaagc caggcacttc tccaaaactc 540
gtgatttatg atacatccaa cctggcttct ggagtcctg ctcgcttcag tggcagtgga 600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat 660
tactgccagc aaagagatag ttaccactc acgttcgggt ctggcaccaa gctggagctg 720
aaacgggcgg ccacacgggt gtcagaaaaa cagctggcgg aggtggtcgc gaatacgatt 780
accocgtga tgaagccca gtctgttcca ggcatggcgg tggccgttat ttatcaggga 840
aaaccgcact attacacatt tggcaaggcc gatatcgcg cgaataaacc cgttacgcct 900
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gccattgtc gcggtgaaat ttcgtggac gatgcggtga ccagatactg gccacagctg 1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacotacac cgctggcggc 1080
ctgccgtac aggtacogga tgaggtoacg gataacgcct cctgtctcg cttttatcaa 1140
aactggcagc cgcagtgaa gcttggcaca acgcgtcttt acgccaacgc cagcatcggt 1200
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aacatggcgc cggagaacgt tgctgatgcc tcacttaagc agggcatcgc gctggcgcag 1500

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cccgtggagg	ccaacacggt	ggcgcgagacg	agttttggta	atgtagcact	ggcgcggtg	1620
cccgtggcag	aagtgaatcc	accggctccc	ccggtcaaa	cgtcctgggt	ccataaaacg	1680
ggctctactg	gcgggttttg	cagctacgtg	gcctttatct	ctgaaaagca	gatcggtatt	1740
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ctcgaggcgc	tacag					1815

<210> 27
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1.6i protein variant

<400> 27	
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cctgaacagg	gcctggagtg gattggatgg attgatcctg agaatggta tactgaatat 180
gccccgaagt	tcacagggca ggccactttt actacagaca cactcctcaa cacagcctac 240
ctgcagctca	gcagcctgac atctgaggac actgcgctct attattgtaa tgaggggctc 300
ccgactgggc	cgtactactt tgactactgg ggccaaggga ccacggctac cgtctcctca 360
gggtggaggcg	gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgtgctcacc 420
cagtctccag	caatcgtgtc tgcactctca ggggagaagg tcaccataac ctgcagtgcc 480
agctcaagtg	taacttacat gcactgggtc cagcagaagc caggcacttc tcccaaacctc 540
gtgatttatg	atacatccaa cctggtctct ggagtccttg ctgcgttcag tggcagtgga 600
tctgggacct	cttactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat 660
tactgccagc	aaagagatag ttaccactc acgttcgggt ctggcaccac gctggagctg 720
aaacggggcg	ccacaccggt gtcagaaaaa cagctggcgg aggtggctgc gaatacagatt 780
accccgctga	tggcggccca gtctgttcca ggcatggcgg tggccgttat ttatcaggga 840
aaaccgcact	attacacatt tggcaaggcc gatatcgcg cgaataaac cgttacgcct 900
cagaccctgt	tcgagctggg ttctataagt aaaaccttca ccggcgcttt agtgggggat 960
gccattgtct	gcggtgaaat ttctgtggac gatgcggtga ccagatactg gccacagctg 1020
acgggcaagc	agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcgcc 1080

```

ctgccgctac aggtaccgga tgaggtaacg gataacgcct cctgctgcg cttttatcaa 1140
aactggcagc cgcagtgga gctgggcaca acgcgtcttt acgccaacgc cagcatcggt 1200
ctttttggtg cgctggcggt caaaccttct ggcattgcct atgagcagc catgacgacg 1260
cggttctcta agcgcgtcaa gctggaccat acctggatta acgtgccgaa agcgggaagag 1320
gcgcattacg cctggggcta tcgtgacggt aaagcgggtg cgttttcgc gggtatgctg 1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaactg ggtcatggca 1440
aacatggcgc cggagaacgt tgctgatgcc tcacttaagc agggcatcgc gctggcgcag 1500
tcgcgctact ggcgatcgcg gtcaatgtat cagggctctg gctgggagat gctcaactgg 1560
cccgtaggag ccaacacggt ggtcgagacg agttttggta atgtagcact ggcgcgcttg 1620
ccctgggcag aagtgaatcc accggctccc ccggtcaaag cgtcctgggt ccataaaacg 1680
ggctctactg cggggttttg cgcgtacgtg gcctttatc ctgaaaagca gatcggtatt 1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatata 1800
ctcgaggcgc tacag 1815

```

```

<210> 28
<211> 771
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> sequence encoding CDRs of CAb1.7 protein variant

```

```

<220>
<221> misc_feature
<222> (1)..(153)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (184)..(225)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (274)..(372)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (406)..(552)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (583)..(627)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (649)..(744)
<223> n = a,t,c, or g

```

```

<400> 28
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 60
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 120
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnggcttca acattaaaga ctctatatg 180
cacnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnntggat tgatcctgag 240
aatggtgata ctgaatatgc cccgaagttc cagnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 300
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 360
nnnnnnnnnnnn nngggctccc gctcggggcc atttacaacg actacnnnnnn nnnnnnnnnnnn 420
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 480
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 540
nnnnnnnnnnnn nnagtgcag ctcagctgta tatgccatgc acnnnnnnnnn nnnnnnnnnnnn 600
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnngat acatccaacc tggcttctnnn nnnnnnnnnnnn 660
nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 720
nnnnnnnnnnnn nnnnnnnnnnnn nnnncagcaa agagatagtt acccactcac g 771

```

```

<210> 29
<211> 1815
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> sequence encoding CAB1.7 protein variant

```

```

<400> 29
cagggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg 60
tcttgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120
cctgaacagg gcctggagtg gattggatgg attgatcctg agaatgtgtg tactgaatat 180
gccccgaagt tccagggc aa ggccactttt actacagaca catcctccaa cacagcctac 240
ctgcagctca gcagcctgac atctgaggac actgcctgtc attattgtaa tgaggggctc 300

```

ccgctcgggg ccatttaca	cgactactgg ggccaaggga	ccacggtcac cgtctcctca	360
ggtggaggcg gttcaggcgg	agggtggctct ggcggtgggc	gatcagaaaa tgtgctcacc	420
cagtctccag caatcgtgtc	tgcactctcca ggggagaagg	tcaccataac ctgcagtgcc	480
agtcacgtg tatatgccat	gcactgggttc cagcagaagc	caggcacttc tcccaaaactc	540
gtgatttatg atacatccaa	cctggcttct ggagtcctg	ctcgcttcag tggcagtgga	600
tctgggacct cttactctct	cacaatcagc cgaatggagg	ctgaagatgc tgccacttat	660
tactgccagc aaagagatag	ttacccaactc acgttcgggt	ctggcaccaa gctggagctg	720
aaacggggcg ccacacccgt	gtcagaaaaa cagctggcgg	agggtggtcg gaatacgatt	780
accccgtga tgaagccca	gtctgttcca ggcattggcg	tggccgttat ttatcaggga	840
aaaccgcact attacacatt	tggcaaggcc gatatcgcg	cgaataaacc cgttacgcct	900
cagacctgt tcgagctggg	ttctataagt aaaaccttca	ccggcgcttt aggtggggat	960
gccattgtct gcggtgaaat	ttcgtgggac gatgcgggtg	ccagatactg gccacagctg	1020
acggggcaag agtggcaggg	tattcgtatg ctggatctcg	ccacctacac cgtcggcggc	1080
ctgccgtac aggtacccga	tgaggtoacg gataacgcct	cctcgtcgcg cttttatcaa	1140
aactggcagc cgcagtggaa	gcctggcaca acgcgtcttt	acgccaacgc cagcatcggt	1200
ctttttggtg cgtcggcggt	caaaccttct ggcatgcct	atgagcagcg catgacgacg	1260
cgggtcctta agccgctcaa	gctggaccat acctggatta	acgtgccgaa agcgaagag	1320
gcgcattacg cctggggcta	tcgtagcggg aaagcgggtc	gcgtttcgcc gggtatgctg	1380
gatgcacaag cctatggcgt	gaaaaccaac gtgcaggata	tggcgaactg ggtcatggca	1440
aacatggcgc cggagaacgt	tgctgatgcc tcacttaagc	agggcactcg gctggcgcag	1500
tcgcgctact ggcgatatcg	gtcaatgtat cagggtctcg	gctgggagat gctcaactgg	1560
cccgtggagg ccaacacggt	ggtcgagacg agttttggta	atgtagcact ggcgcgcttg	1620
cccgtggcag aagtgaatcc	accggctccc ccggtcaaag	cgtcctgggt ccataaaaacg	1680
ggctctactg gcgggttttg	cagctacgtg gcctttatcc	ctgaaaagca gatcgggtatt	1740
gtgatgctcg cgaatacaag	ctatccgaac ccggcacgcg	ttgaggcgcg ataccatatac	1800
ctcgaggcgc tacag			1815

<210> 30
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>

<223> sequence encoding CAB1.7i protein variant

<400> 30

cagggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg	60
tcctgcacag cttctggcct caacattaaa gactcctata tgcactgggt gaggcagggg	120
cctgaacagg gcctggagtg gattggatgg attgatcctg agaatggta tactgaatat	180
gccccgaagt tccagggcaa ggccaacttt actacagaca catcctccaa cacagcctac	240
ctgcagctca gcagcctgac atctgaggac actgccgtct attattgtaa tgaggggctc	300
ccgctcgggg ccattttaca cgactactgg ggccaaggga ccacgggtcac cgtctcctca	360
gggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgtgtccacc	420
cagtctccag caatcgtgtc tgcactctca ggggagaagg tcaccataac ctgcagtgcc	480
agctcagctg tatatgccat gcactgggtc cagcagaagc caggcacttc tcccaaaetc	540
gtgatttatg atacatccaa cctggcttct ggagtcctg ctcgcttcag tggcagtggg	600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tggcacttat	660
tactgccagc aaagagatag ttaccactc acgttcgggt ctggcaccaa gctggagctg	720
aaacggggcg ccacaccggt gtcagaaaaa cagctggcgg aggtggtcgc gaatacgatt	780
accccgctga tggcgggcca gtctgttcca ggcatggcgg tggccgttat ttatcaggga	840
aaaccgcact attacacatt tggcaaggcc gatatcgcg cgaataaacc cgttacgcct	900
cagaccctgt tcgagctggg ttctataagt aaaaccttca ccggcgcttt aggtggggat	960
gccattgtc cgggtgaaat ttcgctggac gatgcggtga ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcggc	1080
ctgocgtac aggtacogga tgaggtcacg gataacgcct cctgctgcg cttttatcaa	1140
aactggcagc cgcagtgtaa gcctggcaca acgcgtcttt acgccaacgc cagcatcggt	1200
ctttttggtg cgctggcggt caaaccttct ggcctgcct atgagcaggc catgacgacg	1260
cggtctctta agccgctcaa gctggaccat acctggatta acgtgccgaa agcgggaagag	1320
gcgcattacg cctggggcta tcgtgacggt aaagcgggtc gcgtttcgcc gggatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaaact ggtcatggca	1440
aacatggcgc cggagaacgt tgctgatgcc tcacttaagc agggcatcgc gctggcgacg	1500
tcgcgctact ggcgtatcgg gtcaatgtat cagggtctgg gctgggagat gctcaactgg	1560

```

cccgtaggagg ccaacacggt ggtcgagacg agttttggta atgtagcact ggcgcgcttg 1620
cccgtaggag aagtgaatcc accggtctcc ccggtcaaaag cgctctgggt ccataaaaagc 1680
ggctctactg gcgggtttgg cgcgtacgtg gcctttatct ctgaaaagca gatcggtatt 1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatatc 1800
ctcgaggcgc tacag 1815

```

```

<210> 31
<211> 771
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> sequence encoding CDRs of CAb1 protein

```

```

<220>
<221> misc_feature
<222> (1)..(153)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (184)..(225)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (274)..(372)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (406)..(552)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (583)..(627)
<223> n = a,t,c, or g

```

```

<220>
<221> misc_feature
<222> (649)..(744)
<223> n = a,t,c, or g

```

```

<400> 31
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 60
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 120
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnngccttca acattaaaga ctctatatg 180

```

cacnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnntggat	tgatcctgag	240
aatgggtgata	ctgaatatgc	cccgaagttc	cagnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	300
nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	360
nnnnnnnnnnnn	nngggactec	gactgggceg	tactactttg	actacnnnnn	nnnnnnnnnnnn	420
nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	480
nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	540
nnnnnnnnnnnn	nnagtgccag	ctcaagtgtg	agttacatgc	acnnnnnnnnnn	nnnnnnnnnnnn	600
nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnagc	acatccaacc	tggtctctnn	nnnnnnnnnnnn	660
nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnnnnnnnn	720
nnnnnnnnnnnn	nnnnnnnnnnnn	nnnnnagcaa	agatctagtt	accactcac	g	771

```

aaaccgcact attacacatt tggcaaggcc gatatcgccg cgaataaacc cgttacgcct 900
cagacctgtg tcgagctggg ttctataagt aaaaccttca ccggcgcttt aggtggggat 960
gccattgctc gcggtgaaat ttcgctggac gatgcggtga ccagatactg gccacagctg 1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcgcc 1080
ctgccgtac aggtaccgga tgaggtoacg gataacgcct ccctgctcgc cttttataca 1140
aactggcagc cgcagtggaa gcctggcaca acgcgtcttt acgccaaacg cagcatcggt 1200
ctttttggtg cgctggcggt caaaccttct ggcatgcct atgagcaggc catgacgacg 1260
cggttcctta agccgcgtcaa gctggaccat acctggatta acgtgccgaa agcggaagag 1320
gcgcattacg cctggggcta tcgtgacggt aaagcggtgc gcgtttcgcc gggtatgctg 1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaaact ggatcaggca 1440
aacatggcgc cggagaacgt tgccgatgcc tcaactaagc agggcatcgc gctggcgcag 1500
tcgcgctact ggcgtatcgg gtcaatgtat cagggtctcg gctgggagat gctcaactgg 1560
cccgtggagg ccaacacggt ggtcgagacg agttttggtg atgtagcact ggcgccgttg 1620
cccgtggcag aagtgaatcc accggctccc ccggtcaaag cgtcctgggt ccataaaaacg 1680
ggctctactg gcgggtttgg cagctacgtg gcctttatct ctgaaaagca gatcggtatt 1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgagggcgc ataccatata 1800
ctcgaggcgc tacag 1815

```

```

<210> 33
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> CDRs of SW149.5 protein

```

```

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> X = any amino acid

```

```

<220>
<221> MISC_FEATURE
<222> (36)..(49)
<223> X = any amino acid

```

```

<220>
<221> MISC_FEATURE

```

<222> (66)..(98)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (110)..(158)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (169)..(183)
<223> X = any amino acid

<220>
<221> MISC_FEATURE
<222> (191)..(222)
<223> X = any amino acid

<400> 33

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45

Xaa Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Xaa Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Ala

145 150 155 160
 Ser Ser Ser Val Ser Tyr Met His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 165 170 175
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Ser Asn Leu Ala Ser Xaa Xaa
 180 185 190
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 210 215 220
 Arg Asp Ser Tyr Pro Leu Thr
 225 230

<210> 34
 <211> 771
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CDRs of SW149.4 protein

<220>
 <221> misc_feature
 <222> (1)..(153)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (184)..(225)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (274)..(372)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (406)..(552)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (583)..(627)
 <223> n = a,t,c, or g

<220>
 <221> misc_feature
 <222> (649)..(744)
 <223> n = a,t,c, or g

<400> 34
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 60
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 120
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnggcttca acattaaaga ctctatatg 180
 caennnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnntggat tgatcctgag 240
 aatggtgata ctgaatatgc cccgaagttc cagnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 300
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 360
 nnnnnnnnnnnn nnnnggctccc gctcggggcc atttacaacg actacnnnnnn nnnnnnnnnnnn 420
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 480
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 540
 nnnnnnnnnnnn nnnagtccag ctcaagtgtg agttacatgc acnnnnnnnnn nnnnnnnnnnnn 600
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnngat acatccaacc tggcttctnnn nnnnnnnnnnnn 660
 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn 720
 nnnnnnnnnnnn nnnnnnnnnnnn nnnncagcaa agagatagtt acccactcac g 771

<210> 35
 <211> 18:5
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding SW149.5 protein

<400> 35
 caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg 60
 tctctgcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120
 cctgaacagg gcctggatg gattggatgg attgatcctg agaatgtga tactgaatat 180
 gcccccagat tccagggc aa ggccactttt actacagaca catcctccaa cacagcctac 240
 ctgcagctca gacgcctgac atctgaggac actgcccgtct attattgtaa tgaggggctc 300
 ccgctcgggg ccatttaca cgaactactgg ggccaaggga ccacggtcac cgtctcctca 360
 ggtggaggcg gttcaggcg aggtggctct ggcgggtggcg gatcagaaaa tgtgtccacc 420
 cagtctccag caatcgtgtc tgcattctca ggggagaagg tcaccataac ctgcagtgcc 480

agotcaagtg taagttacat gcaactgggtc cagcagaagc caggcacttc tcccaaaactc	540
gtgatttatg atacatccaa cctggcttct ggagtcctcg ctgcgttcag tggcagtgga	600
tctgggacct ctactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat	660
tactgcagc aaagagatag ttaccacactc acgttcgggt ctggccacaa gctggagctg	720
aaacggggcg ccacacccgt gtcagaaaaa cagctggcgg agtggtgcgc gaatacgatt	780
accccgctga tgaagccca gtctgttcca ggcctggcgg tggcogttat ttatcaggga	840
aaaccgcact attacacatt tggcaaggcc gatatcgcg cgaataaacc cgttacgcct	900
cagaccctgt tcgagctggg ttctataagt aaaaccttca ccggcgtttt aggtggggat	960
gccattgctc gcggtgaaat ttcgctggac gatgcgggtg ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcggc	1080
ctgccgtac aggtaccgga tgaggtoacg gataacgcct cctgctgcgc cttttatcaa	1140
aactggcagc cgcagtgga gcttggcaca acgcgtcttt acgccaacgc cagcatcggt	1200
ctttttggtg cgctggcggt caaaccttct ggcatgcct atgagcaggc catgacgacg	1260
cggttcctta agccgctcaa gctggacat acctggatta acgtgccgaa agcggaagag	1320
gcgcattacg cctggggcta tcgtgacggt aaagcgggtc gcgtttcgcc gggtatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaaactg ggtcatggca	1440
aacatggcgc cggagaacgt tgctgatgac tcaactaagc agggcatcgc gctggcgcag	1500
tcgcgctact ggcgatcgg gtcaatgtat cagggtctgg gctgggagat gctcaactgg	1560
cccgtggagg ccaacacggt ggtcgagacg agttttggt atgtagcact ggcgcggtg	1620
cccgtggcag aagtgaatcc accggctccc ccggtcaaag cgtcctgggt ccataaaacg	1680
ggctctactg gcgggtttgg cagctacgtg gcctttatc ctgaaaagca gatcggtatt	1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatata	1800
ctcgaggcgc tacag	1815

<210> 36
 <211> 1083
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sequence encoding BLA protein

 <400> 36

acaccggtgt	cagaaaaaca	gctggcggag	gtggtcgcga	atacgattac	cccgtgatg	60
aaagccagct	ctgttcacag	catggcgggtg	gccgttattt	atcaggga	accgactat	120
tacacatttg	gaaaggccga	tatgcggcgg	aataaacccg	ttacgcctca	gaccctgttc	180
gagctgggtt	ctataagtaa	aaccttcacc	ggcggttttag	gtggggatgc	cattgctcgc	240
ggtgaaattt	cgttggaaga	tgcggtgacc	agatactggc	cacagctgac	gggcaagcag	300
tggcagggtg	ttcgtatgct	ggatctcgcc	acctacaccg	ctggcggcct	gccgctacag	360
gtaccggatg	aggtaacgga	taacgcctcc	ctgctcgcgt	tttatcaaaa	ctggcagccg	420
cagtggaaac	ctggcacaac	gcgtctttac	gccaacgccca	gcacggctct	ttttggtgcg	480
ctggcgggtc	aaactttctg	catgccctat	gagcaggcca	tgacgacgcg	ggcctttaag	540
ccgctcaaac	tggaccatac	ctggattaac	gtgccgaaaag	cggaaaggcg	gcattacgcc	600
tggggctatc	gtgacggtaa	agcggtgccg	gtttcgccgg	gtatgtcgga	tgacaagccc	660
tatggcgtga	aaaccaacgt	gcaggatatg	gcgaactggg	tcattggcaaa	catggcgccg	720
gagaacgttg	ctgatgcctc	acttaagcag	ggcatcgccg	tggcgacgtc	ggcctactgg	780
cgtatcggtt	caatgtatca	gggtctgggc	tgggagatgc	tcaactggcc	cgtggaggcc	840
aacacggtgg	tcgagacgag	tttttgtaat	gtagactcgg	cgccgctgcc	cgtggcagaa	900
gtgaatccac	cggctccccc	ggtaaaagcg	tctgggtccc	ataaaacggg	ctctactggc	960
gggtttggca	gctactgtgc	ctttattcct	gaaaagcaga	tcggatttgt	gatgctcgcg	1020
aatacaagct	atccgaaccc	ggcagcgcgt	gaggcggcat	accatatcct	cgaggcgcta	1080
cag						1083

<210> 37
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1.1 protein variant

<400> 37	
caggtgaaac	tcgacagctc
tctgcacag	ctttctggtt
cctgaacagg	gcctggagtg
gccccgaagt	tcaggggcaa
ctgcagctca	gcagcctgac
	atctgaggac
	actgccgtct
	attattgtaa
	tgaggggact
	60
	120
	180
	240
	300

ccgactgggc cgtactactt tgactactgg ggccaaggga ccacggtcac cgtctcctca	360
gggtggaggcg gttcaggcgg aggtggctct ggcggtggcg gatcagaaaa tgtgtccacc	420
cagtctccag caatcatgtc tgcattctca ggggagaagg tcaccataac ctgcagtgcc	480
agctcaagtg taagtacatg cactctgggtc cagcagaagc caggcacttc tccaaaactc	540
gtgattata gacatccaa cctggcttct ggagtcctcg ctgcgttcag tggcagtgga	600
tctgggacct ttactctct cacaatcagc cgaatggagg ctgaagatgc tgccacttat	660
tactgccagc aaagatctag ttaccactc acgttcgggt ctggcaccaa gctggagctg	720
aaacgggcgg ccacacccgt gtcagaaaaa cagctggcgg aggtggctgc gaatacagatt	780
accccgcctg tgaaagccca gtctgttcca ggcatggcgg tggccgttat ttatcaggga	840
aaaccgcact attacacatt tggcaaggcc gatatcgccg cgaataaacc cgttacgcct	900
gagacctgt tcgagctggg ttctataagt aaaaccttca ccggcgcttt aggtggggat	960
gccattgtc cgggtgaaat ttcgctggac gatgcgggtg ccagatactg gccacagctg	1020
acgggcaagc agtggcaggg tattcgtatg ctggatctcg ccacctacac cgctggcggc	1080
ctgccgctac aggtaccgga tgaggtoacg gataacgcct ccctgctcgc cttttatcaa	1140
aactggcagc cgcagtgga gctgggaca acgcgtcttt acgccaacgc cagcatcggt	1200
ctttttggtg cgctggcggt caaaccttct ggcatgcct atgagcaggc catgacgacg	1260
cgggtcctta agccgctcaa gctggaacct acctggatta acgtgccgaa agcgggaagag	1320
gcgcattacg cctggggcta tcgtgacggt aaagcgggtc gcgtttcgcc gggatatgctg	1380
gatgcacaag cctatggcgt gaaaaccaac gtgcaggata tggcgaactg ggtcatggca	1440
aacatggcgc cggagaacgt tgctgatgcc tcacttaagc agggcatcgc gctggcgcag	1500
tcgcgctact ggcgatcgg gtcaatgtat cagggtctg gctgggagat gtcgaactgg	1560
cccgtggagg ccaacacggt ggtcgagacg agttttggta atgtagcact ggcgccgttg	1620
cccgtggcag aagtgaatcc accggctccc ccggtcaaa cgtcctgggt ccataaaacg	1680
ggctctactg gcgggttttg cagctacgtg gcctttatct ctgaaaagca gatcgggtatt	1740
gtgatgctcg cgaatacaag ctatccgaac ccggcacgcg ttgaggcggc ataccatata	1800
ctcgaggcgc tacag	1815

<210> 38
 <211> 605
 <212> PRT

<213> Artificial Sequence

<220>

<223> CAB1.2i protein variant

<400> 38

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln
405 410 415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
 435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
 450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
 465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
 485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
 500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
 515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
 530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
 545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys
 565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
 580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
 595 600 605

<210> 39
 <211> 1815
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1.2i protein variant

<400> 39
 caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg 60
 tctctcacag cttctggctt caacattaaa gactcctata tgcactgggt gaggcagggg 120

cctgaacagg	gcctggagtg	gattggatgg	attgatcctg	agaatggtga	tactgaatat	180
gccccgaagt	tccaggggcaa	ggccactttt	actacagaca	catcctccaa	cacagcctac	240
ctgcagctca	gcagcctgac	atctgaggac	actgccgtct	attattgtaa	tgaggggact	300
ccgactgggc	cgtactactt	tgactactgg	ggccaaggga	ccacggtcac	cgtctcctca	360
ggtggaggcg	gttcaggcgg	agggtgctct	ggcggtggcg	gacagaaaa	tgtgctcacc	420
cagtctccag	caatcgtgtc	tgcattctca	ggggagaagg	tcaccataac	ctgcagtgcc	480
agctcaagt	taagttacat	gcactgggtc	cagcagaagc	caggcacttc	tcocaaactc	540
gtgatttata	gcacatccaa	cctggcttct	ggagtcctcg	ctcgcctcag	tggcagtggg	600
tctgggacct	cttactctct	cacaatcagc	cgaatggagg	ctgaagatgc	tgccacttat	660
tactgccagc	aaagatctag	ttaccacttc	acgttcgggt	ctggccacaa	gctggagctg	720
aaacggggcg	ccacaccggt	gtcagaaaa	cagctggcgg	agggtgtcgc	gaatacgatt	780
accocgctga	tggcgcccaa	gtctgttcca	ggcatggcgg	tggccgttat	ttatcaggga	840
aaaccgcact	attacacatt	tggcaaggcc	gatatcgccg	cgaataaacc	cgttacgcct	900
cagaccctgt	tcgagctggg	ttctataagt	aaaaccttca	ccggcgtttt	agggtgggat	960
gccattgctc	gcggtgaaat	ttcgctggac	gatgcggtga	ccagatactg	gccacagctg	1020
acgggcaagc	agtggcaggg	tattcgtatg	ctggatctcg	ccacctacac	cgtcggcggc	1080
ctgcgcgtac	aggtaaccga	tgaggtoacg	gataacgcct	cctcgtcgcg	cttttatcaa	1140
aaactggcagc	cgcagtgga	gcctggcaca	acgcgtcttt	acgccaaacg	cagcatcggt	1200
ctttttggtg	cgcgtggcgt	caaaccttct	ggcatgccct	atgagcaggc	catgacgacg	1260
cgggtcctta	agccgcotca	gctgggacat	acctggatta	acgtgccgaa	agcgggaagag	1320
gcgcattacg	cctggggcta	tcgtgacggt	aaagcgggtc	gcgtttcgcc	gggtatgctg	1380
gatgcacaag	cctatggcgt	gaaaaccaac	gtgcaggata	tggcgaaactg	ggatcaggca	1440
aacatggcgc	cggagaacgt	tgcgtgatgc	tcacttaagc	agggcatacg	gctggcgcag	1500
tcgcgtact	ggcgatcgg	gtcaatgtat	cagggtctcg	gctgggagat	gtcgaactgg	1560
cccgtggagg	ccaacacggt	ggtcgagacg	agttttggtg	atgtagcact	gccgcggttg	1620
cccgtggcag	aagtgaatcc	accggctccc	ccggtcaaa	cgtcctgggt	ccataaaacg	1680
ggctctactg	gcgggttttg	gcgctacgtg	gcctttattc	ctgaaaagca	gatcgggtatt	1740
gtgatgctcg	cgaataaca	ctatccgaac	ccggcacgcg	ttgaggcggc	ataccatatc	1800

<210> 40
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB1.13i protein variant

<400> 40

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Ser Gly Gly
1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50 55 60

Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Asn Glu Gly Leu Pro Leu Gly Ala Ile Tyr Asn Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
130 135 140

Ile Val Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
145 150 155 160

Ser Ser Ala Val Tyr Ala Met His Trp Phe Gln Gln Lys Pro Gly Thr
165 170 175

Ser Pro Lys Leu Val Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
180 185 190

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
195 200 205

Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Arg Asp Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
225 230 235 240

Lys Arg Ala Ala Thr Pro Val Ser Glu Lys Gln Leu Ala Glu Val Val
245 250 255

Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro Gly Met
260 265 270

Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly
275 280 285

Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe
290 295 300

Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp
305 310 315 320

Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr
325 330 335

Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp
340 345 350

Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu
355 360 365

Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro
370 375 380

Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser Ile Gly
385 390 395 400

Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln

405

410

415

Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp
 420 425 430

Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg
 435 440 445

Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala
 450 455 460

Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val Met Ala
 465 470 475 480

Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln Gly Ile
 485 490 495

Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly
 500 505 510

Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr Val Val
 515 520 525

Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu
 530 535 540

Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His Lys Thr
 545 550 555 560

Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro Glu Lys
 565 570 575

Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala
 580 585 590

Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
 595 600 605

<210> 41
 <211> 1814
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> sequence encoding CAB1.13i protein variant

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<400> 41
caggtgcagc tgcagcagtc tggggcagaa cttgtgaaat cagggggctc agtcaagttg    60
tcttcacacag cttctggcct caacattaaa gactcctata tgcactgggt gaggcagggg    120
cctgaacagg gcctggagtg gattggatgg attgatcctg agaatggta tactgaatat    180
gccccgaagt tccagggcga ggccactttt actacagaca catcctccaa cacagcctac    240
ctgcagctca gcagcctgac atctgaggac actgcctgtc attattgtaa tgaggggctc    300
ccgctcgggg ccatttacaa cgactactgg ggccaaggga ccacggtcac cgtctcctca    360
ggtggaggcg gttcaggcgg aggtggctct ggcgggtggc gatcagaaaa tgtgtcacc    420
cagtctccag caatcgtgtc tgcactccca ggggagaagg tcaccataac ctgcagtgcc    480
agctcagctg tatatgccat gcactgggtc cagcagaagc caggcacttc tccaaaactc    540
gtgatttata gcacatccaa cctggcttct ggagtccttg ctgcgttcag tggcagtggg    600
tctgggacct cttactctct cacaatcagc cgaatggagg ctgaagatgc tggcacttat    660
tactgccagg aaagagatag ttaccactc acgttcgggt ctggccacca gctggagctg    720
aaacgggcgg ccacaccggt gtcagaaaaa cagctggcgg aggtggctgc gaatacgatt    780
accocgctga tggcggccca gtctgttcca ggcatggcgg tggccgttat ttatcaggga    840
aaaccgcact attacacatt tggcaaggcc gatatcgccg cgaataaacc cgttacgcct    900
cagaccctgt togagctggg ttctataagt aaaaccttca ccggcgcttt ggtggggatg    960
ccattgctcg cggtgaaatt tcgctggacg atgcggtgac cagatactgg ccacagctga   1020
cgggcaagca gtggcagggt attcgtatgc tggatctcgc cacctacacc gctggcggcc   1080
tgccgctaca ggtaccggat gaggtcacgg ataacgcctc cctgctgcgc ttttatcaaa   1140
actggcagcc gcagtggaag cctggcacia cgcgtcttta cgccaacgcc agcatcggtc   1200
tttttggtgc gctggcggtc aaacctctgt gcatgcccta tgagcagccc atgacgacgc   1260
gggtccttaa gccgctcaag ctggaccata cctggattaa cgtgccgaaa gcggaagagg   1320
cgcattacgc ctggggctat cgtgacggta aagcggtgcg cgtttcgccg ggtatgctgg   1380
atgcacaagc ctatggcgtg aaaaccaacg tgcaggatat ggcgaaactgg gtcattggcaa   1440
acatggcgcc ggagaacgtt gctgatgcct cacttaagca gggcatcgcg ctggcgcagt   1500
cgcgctactg cgtatcggg tcaatgtatc agggctctgg ctgggagatg ctcaactggc   1560
ccgtggaggc caacacggtg gtcgagacga gttttggtaa tgtagcactg gcgccgttgc   1620
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ccgtggcaga agtgaatcca ccggtccccc cgggtcaaagc gtctctgggtc cataaaacgg 1680
 gctctactgg cgggttttggc gcgtacgtgg cctttatttc tgaaaagcag atcggtattg 1740
 tgatgctcgc gaatacaagc tatccgaacc cggcacgcgt tgaggcggca taccatatcc 1800
 tcgaggcgct acag 1814

<210> 42
 <211> 623
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> CAB1.13i protein variant
 <400> 42

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
 20 25 30

Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
 35 40 45

Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
 50 55 60

Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Asp
 65 70 75 80

Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
 85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
 100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 130 135 140

Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys
 145 150 155 160

Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
165 170 175

Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
180 185 190

Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
195 200 205

Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
210 215 220

Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225 230 235 240

Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
245 250 255

Ser Val Thr Val Ser Ser Thr Pro Val Ser Glu Lys Gln Leu Ala Glu
260 265 270

Val Val Ala Asn Thr Ile Thr Pro Leu Met Ala Ala Gln Ser Val Pro
275 280 285

Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr
290 295 300

Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr
305 310 315 320

Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly
325 330 335

Gly Asp Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr
340 345 350

Arg Tyr Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met
355 360 365

Leu Asp Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro
370 375 380

Asp Glu Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp
385 390 395 400

Gln Pro Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser
405 410 415

Ile Gly Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr
420 425 430

Glu Gln Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His
435 440 445

Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly
450 455 460

Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala
465 470 475 480

Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val
485 490 495

Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln
500 505 510

Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr
515 520 525

Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr
530 535 540

Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val
545 550 555 560

Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His
565 570 575

Lys Thr Gly Ser Thr Gly Gly Phe Gly Ala Tyr Val Ala Phe Ile Pro
580 585 590

Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn
595 600 605

Pro Ala Arg Val Glu Ala Ala Tyr His Ile Leu Glu Ala Leu Gln
 610 615 620

<210> 43
 <211> 1869
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence encoding CAB1.11i protein variant

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<400> 43
gacatcgtcc tgacccagag cccggcaagc ctgtctgttt cctggggcca gcgtgccact    60
atgtcctgca gagcgggtga gtctgttgac attttcggtg tcggttttct gcactgggtac    120
caacagaaac cgggtcagcc gccaaaactg ctgattctatc gtgcttctaa cctggagtc    180
ggcatcccg   tacgtttctc cggtagctgg tctggtagct attttaccct gattatcgac    240
ccggtggaag cagacgatgt tgccacctac tattgccagc agaccaacga ggatccgtac    300
accttcggtg cgggtactaa actggagatc aaaggcgggt gtgggtcttg tggtgggtgg    360
agcgggtggc gtggtagcgg tggcggtagc agcgggtggt gtggctctgg tggcgggtgg    420
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